



S1 Fig. A. Distribution of mCSM-PPI2¹³ predicted $\Delta\Delta G$ from *in silico* saturation mutagenesis of the ACE2-S interface in PDB 6vw1¹¹. A. predicted $\Delta\Delta G$ for 475 mutations across 25 sites on ACE2 corresponding to the 23 residues within 5 Å of SARS-CoV-2 S plus Gly326 and Gly352. B. predicted $\Delta\Delta G$ for the subset of 151 mutations across these sites that are accessible via a single base change of the ACE2 coding sequence.